

SEQUENCE LISTING

<110> Kindl, Helmut
 May, Christian
 Feussner, Ivo

<120> The N-terminal beta-barrel structure of lipid body lipoxxygenase mediates
 its binding to liposomes and lipid bodies

<130> 99_1235

<140> US 10/089,147

<141> Filing date not yet granted

<150> PCT/EP/00/09912

<151> 2000-10-10

<160> 4

<170> WordPerfect 6.1

<210> 1

<211> 732

<212> DNA

<213> Cucumis sativus

<220>

<221> CDS

<222> (1)..(732)

<400> 1

atg ttt gga att ggg aag aac atc att gaa ggg gcc ttg aat aca act	48
Met Phe Gly Ile Gly Lys Asn Ile Ile Glu Gly Ala Leu Asn Thr Thr	
1 5 10 15	
gga gat ctt gca ggt tct gtt atc aat gct ggt ggt aac att tta gat	96
Gly Asp Leu Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp	
20 25 30	
aga gtt tcc agt ctt gga gga aac aaa atc aaa ggg aaa gtg att ctt	144
Arg Val Ser Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu	
35 40 45	
atg aga agc aat gtt ttg gat ttc act gaa ttt cat tcc aat ctt ctt	192
Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu	
50 55 60	
gat aac ttc act gag ctc ttg ggt ggt ggt gtt tct ttc caa ctc att	240
Asp Asn Phe Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile	
65 70 75 80	
agt gcc act cat act tca aat gac tca aga ggg aaa gtt ggg aac aag	288
Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys	
85 90 95	

gca tat ttg gag agg tgg cta act tca atc cca cca ctg ttt gct gga 336
 Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly
 100 105 110

gaa tca gtg ttc caa atc aac ttt caa tgg gat gaa aat ttt gga ttt 384
 Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe
 115 120 125

cca gga gct ttc ttc ata aaa aat gga cat aca agt gaa ttc ttt ctc 432
 Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
 130 135 140

aaa tct ctc act ctt gat gat gtt cct ggc tat ggc aga gtc cat ttt 480
 Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe
 145 150 155 160

gat tgc aat tct tgg gtt tac cct tct gga aga tac aag aaa gat cgc 528
 Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg
 165 170 175

att ttc ttt gcc aat cat gtt tat ctt cca agt caa aca cca aac cct 576
 Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro
 180 185 190

ctt cgt aag tat aga gag gaa gaa ttg tgg aat ttg aga gga gat gga 624
 Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly
 195 200 205

aca gga gaa aga aag gaa tgg gat aga att tat gac tat gat gtt tat 672
 Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr
 210 215 220

aat gac att gct gac cct gat gtt ggt gat cat cgt cct att ctc ggt 720
 Asn Asp Ile Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly
 225 230 235 240

ggg acg acc gaa 732
 Gly Thr Thr Glu

<210> 2
 <211> 244
 <212> PRT
 <213> Cucumis sativus

<400> 2

Met Phe Gly Ile Gly Lys Asn Ile Ile Glu Gly Ala Leu Asn Thr Thr
 1 5 10 15

Gly Asp Leu Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp
 20 25 30

Arg Val Ser Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu
 35 40 45

Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu
50 55 60

Asp Asn Phe Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile
65 70 75 80

Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys
85 90 95

Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly
100 105 110

Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe
115 120 125

Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
130 135 140

Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe
145 150 155 160

Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg
165 170 175

Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro
180 185 190

Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly
195 200 205

Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr
210 215 220

Asn Asp Ile Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly
225 230 235 240

Gly Thr Thr Glu

<210> 3

<211> 2964

<212> DNA

<213> Cucumis sativus

<220>

<221> CDS

<222> (48)..(2684)

<400> 3

gttccaaaca cacagtgagc aaaaaagaaa agtaaaaaag agtgaaa atg ttt gga 56
Met Phe Gly
1

att ggg aag aac atc att gaa ggg gcc ttg aat aca act gga gat ctt 104
Ile Gly Lys Asn Ile Ile Glu Gly Ala Leu Asn Thr Thr Gly Asp Leu
5 10 15

gca ggt tct gtt atc aat gct ggt ggt aac att tta gat aga gtt tcc	152
Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp Arg Val Ser	
20 25 30 35	
agt ctt gga gga aac aaa atc aaa ggg aaa gtg att ctt atg aga agc	200
Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu Met Arg Ser	
40 45 50	
aat gtt ttg gat ttc act gaa ttt cat tcc aat ctt ctt gat aac ttc	248
Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu Asp Asn Phe	
55 60 65	
act gag ctc ttg ggt ggt ggt gtt tct ttc caa ctc att agt gcc act	296
Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile Ser Ala Thr	
70 75 80	
cat act tca aat gac tca aga ggg aaa gtt ggg aac aag gca tat ttg	344
His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys Ala Tyr Leu	
85 90 95	
gag agg tgg cta act tca atc cca cca ctg ttt gct gga gaa tca gtg	392
Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly Glu Ser Val	
100 105 110 115	
ttc caa atc aac ttt caa tgg gat gaa aat ttt gga ttt cca gga gct	440
Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe Pro Gly Ala	
120 125 130	
ttc ttc ata aaa aat gga cat aca agt gaa ttc ttt ctc aaa tct ctc	488
Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu Lys Ser Leu	
135 140 145	
act ctt gat gat gtt cct ggc tat ggc aga gtc cat ttt gat tgc aat	536
Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe Asp Cys Asn	
150 155 160	
tct tgg gtt tac cct tct gga aga tac aag aaa gat cgc att ttc ttt	584
Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg Ile Phe Phe	
165 170 175	
gcc aat cat gtt tat ctt cca agt caa aca cca aac cct ctt cgt aag	632
Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro Leu Arg Lys	
180 185 190 195	
tat aga gag gaa gaa ttg tgg aat ttg aga gga gat gga aca gga gaa	680
Tyr Arg Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly Thr Gly Glu	
200 205 210	
aga aag gaa tgg gat aga att tat gac tat gat gtt tat aat gac att	728
Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr Asn Asp Ile	
215 220 225	
gct gac cct gat gtt ggt gat cat cgt cct att ctc ggt ggg acg acc	776
Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly Gly Thr Thr	
230 235 240	

gaa tat cct tac cct cgt agg gga aga aca gga cga cca cga tca aga	824
Glu Tyr Pro Tyr Pro Arg Arg Gly Arg Thr Gly Arg Pro Arg Ser Arg	
245 250 255	
aga gac cac aat tat gag agc aga ttg tca cca ata atg agc tta gac	872
Arg Asp His Asn Tyr Glu Ser Arg Leu Ser Pro Ile Met Ser Leu Asp	
260 265 270 275	
atc tat gta cca aaa gat gaa aac ttt ggg cat ttg aag atg tca gat	920
Ile Tyr Val Pro Lys Asp Glu Asn Phe Gly His Leu Lys Met Ser Asp	
280 285 290	
ttc ctt ggt tat aca tta aaa gca ctt tgc ata tca atc aaa cca gga	968
Phe Leu Gly Tyr Thr Leu Lys Ala Leu Ser Ile Ser Ile Lys Pro Gly	
295 300 305	
ctt caa tcc ata ttt gat gta act cca aat gaa ttt gac aat ttt aaa	1016
Leu Gln Ser Ile Phe Asp Val Thr Pro Asn Glu Phe Asp Asn Phe Lys	
310 315 320	
gaa gtt gat aat ctc ttt gag aga ggt ttt ccc att cca ttt aat gct	1064
Glu Val Asp Asn Leu Phe Glu Arg Gly Phe Pro Ile Pro Phe Asn Ala	
325 330 335	
ttt aag acc ctc act gag gac ctc act cca cct ttg ttc aaa gca ctc	1112
Phe Lys Thr Leu Thr Glu Asp Leu Thr Pro Pro Leu Phe Lys Ala Leu	
340 345 350 355	
gtg agg aat gat ggt gaa aaa ttc ctc aaa ttt cct act ccc gaa gtt	1160
Val Arg Asn Asp Gly Glu Lys Phe Leu Lys Phe Pro Thr Pro Glu Val	
360 365 370	
gtc aaa gat aat aaa ata gga tgg agc act gat gaa gaa ttt gca aga	1208
Val Lys Asp Asn Lys Ile Gly Trp Ser Thr Asp Glu Glu Phe Ala Arg	
375 380 385	
gaa atg tta gca gga ccc aat cct cta ttg att cgt cgt ctt gaa gct	1256
Glu Met Leu Ala Gly Pro Asn Pro Leu Leu Ile Arg Arg Leu Glu Ala	
390 395 400	
ttt cca cca aca agt aag ctt gac cca aat gtt tat ggg aat caa aac	1304
Phe Pro Pro Thr Ser Lys Leu Asp Pro Asn Val Tyr Gly Asn Gln Asn	
405 410 415	
agt acc atc act gaa gaa cac ata aag cat ggt tta gat ggt ctt acg	1352
Ser Thr Ile Thr Glu Glu His Ile Lys His Gly Leu Asp Gly Leu Thr	
420 425 430 435	
gtt gat gag gca atg aag caa aac agg ctc tac ata gtg gat ttc cat	1400
Val Asp Glu Ala Met Lys Gln Asn Arg Leu Tyr Ile Val Asp Phe His	
440 445 450	
gat gca tta atg ccc tat ctt aca agg atg aat gca aca tca aca aaa	1448
Asp Ala Leu Met Pro Tyr Leu Thr Arg Met Asn Ala Thr Ser Thr Lys	
455 460 465	

aca tat gcc aca aga aca ttg ctt ctt ttg aaa gat gat ggg act ttg	1496
Thr Tyr Ala Thr Arg Thr Leu Leu Leu Leu Lys Asp Asp Gly Thr Leu	
470 475 480	
aag cca ttg gtt att gag tta gcc ttg cca cat cct caa gga gat caa	1544
Lys Pro Leu Val Ile Glu Leu Ala Leu Pro His Pro Gln Gly Asp Gln	
485 490 495	
ctt ggt gcc att agc aaa cta tac ttt cca gct gaa aat gga gtt caa	1592
Leu Gly Ala Ile Ser Lys Leu Tyr Phe Pro Ala Glu Asn Gly Val Gln	
500 505 510 515	
aaa tcc att tgg caa ttg gct aaa gct tat gta act gtt aat gat gtt	1640
Lys Ser Ile Trp Gln Leu Ala Lys Ala Tyr Val Thr Val Asn Asp Val	
520 525 530	
ggc tac cat caa ctt att agt cat tgg ttg cat act cat gct gta ctt	1688
Gly Tyr His Gln Leu Ile Ser His Trp Leu His Thr His Ala Val Leu	
535 540 545	
gag cca ttt gtg att gca aca cat aga caa ttg agc gtg ctt cat cca	1736
Glu Pro Phe Val Ile Ala Thr His Arg Gln Leu Ser Val Leu His Pro	
550 555 560	
atc cat aag ttg ctt gtt cct cat tac aaa gac act atg ttt ata aat	1784
Ile His Lys Leu Leu Val Pro His Tyr Lys Asp Thr Met Phe Ile Asn	
565 570 575	
gca tct gca aga caa gtt ttg atc aat gcc aat ggt ctt atc gaa aca	1832
Ala Ser Ala Arg Gln Val Leu Ile Asn Ala Asn Gly Leu Ile Glu Thr	
580 585 590 595	
acc cat tat cca tca aaa tat tca atg gag ttg tca tct atc ttg tac	1880
Thr His Tyr Pro Ser Lys Tyr Ser Met Glu Leu Ser Ser Ile Leu Tyr	
600 605 610	
aag gat tgg acc ttc cct gat caa gca tta cct aat aat ctc atg aag	1928
Lys Asp Trp Thr Phe Pro Asp Gln Ala Leu Pro Asn Asn Leu Met Lys	
615 620 625	
aga gga cta gct gtg gag gac tca agt gcc ccc cat gga ctt aga ttg	1976
Arg Gly Leu Ala Val Glu Asp Ser Ser Ala Pro His Gly Leu Arg Leu	
630 635 640	
cta ata aat gat tat cca ttt gct gtt gat ggt ctt gac att tgg tca	2024
Leu Ile Asn Asp Tyr Pro Phe Ala Val Asp Gly Leu Asp Ile Trp Ser	
645 650 655	
gcc att aaa aca tgg gta cag gat tat tgc tgt ctc tac tac aaa gat	2072
Ala Ile Lys Thr Trp Val Gln Asp Tyr Cys Cys Leu Tyr Tyr Lys Asp	
660 665 670 675	
gac aat gca gta caa aat gac ttt gaa ctc caa tct tgg tgg aat gag	2120
Asp Asn Ala Val Gln Asn Asp Phe Glu Leu Gln Ser Trp Trp Asn Glu	
680 685 690	

cta aga gag aaa ggc cac gct gac aag aaa cat gaa cca tgg tgg cca	2168
Leu Arg Glu Lys Gly His Ala Asp Lys Lys His Glu Pro Trp Trp Pro	
695 700 705	
aaa atg caa act tta agt gaa tta atc gaa tcc tgc act aca att ata	2216
Lys Met Gln Thr Leu Ser Glu Leu Ile Glu Ser Cys Thr Thr Ile Ile	
710 715 720	
tgg att gct tca gct ctt cat gcc gca gtt aac ttt gga caa tat ccc	2264
Trp Ile Ala Ser Ala Leu His Ala Ala Val Asn Phe Gly Gln Tyr Pro	
725 730 735	
tac gga ggc tat att ctc aat cga cca act aca agt cgt agg ttc atg	2312
Tyr Gly Gly Tyr Ile Leu Asn Arg Pro Thr Thr Ser Arg Arg Phe Met	
740 745 750 755	
cct gaa gtt ggc acg gct gag tac aaa gaa ctg gaa tgc aat ccc gaa	2360
Pro Glu Val Gly Thr Ala Glu Tyr Lys Glu Leu Glu Ser Asn Pro Glu	
760 765 770	
aaa gct ttc ttg aga aca ata tgt tca gaa tta caa gca ctt gtt agt	2408
Lys Ala Phe Leu Arg Thr Ile Cys Ser Glu Leu Gln Ala Leu Val Ser	
775 780 785	
att tca att att gaa atc ttg tca aag cat gct tct gat gaa gtt tat	2456
Ile Ser Ile Ile Glu Ile Leu Ser Lys His Ala Ser Asp Glu Val Tyr	
790 795 800	
ctt gga caa aga gct tca att gat tgg act tca gat aaa att gca ttg	2504
Leu Gly Gln Arg Ala Ser Ile Asp Trp Thr Ser Asp Lys Ile Ala Leu	
805 810 815	
gaa gca ttt gag aaa ttt ggg aaa aat tta ttt gaa gtt gag aat agg	2552
Glu Ala Phe Glu Lys Phe Gly Lys Asn Leu Phe Glu Val Glu Asn Arg	
820 825 830 835	
atc atg gaa agg aat aaa gag gtg aat ttg aag aat aga tct gga cct	2600
Ile Met Glu Arg Asn Lys Glu Val Asn Leu Lys Asn Arg Ser Gly Pro	
840 845 850	
gtt aat ttg cct tat act cta ctt gtt cca tca agt aac gaa gga ctc	2648
Val Asn Leu Pro Tyr Thr Leu Leu Val Pro Ser Ser Asn Glu Gly Leu	
855 860 865	
act gga aga gga att cct aat agt att tct atc taa gttgataaga	2694
Thr Gly Arg Gly Ile Pro Asn Ser Ile Ser Ile	
870 875	
aagaaaagtg gttcttttta tgggtgacgt gtgtaatttg aaggtcacaa attacatttt	2754
aagttgcccc cattattatt atgaaggaaa taaatgacca tatttttagt ttaatttaaa	2814
ttaggtagct atagccaact ttaggctctg ttggatttgg aactatctcc aacttatata	2874
tgtactttgt actactatatt gatgaataaa agttgtgtgt cttagaata aaaaaaaaaa	2934

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa

2964

<210> 4

<211> 878

<212> PRT

<213> Cucumis sativus

<400> 4

Met Phe Gly Ile Gly Lys Asn Ile Ile Glu Gly Ala Leu Asn Thr Thr
 1 5 10 15

Gly Asp Leu Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp
 20 25 30

Arg Val Ser Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu
 35 40 45

Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu
 50 55 60

Asp Asn Phe Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile
 65 70 75 80

Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys
 85 90 95

Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly
 100 105 110

Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe
 115 120 125

Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
 130 135 140

Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe
 145 150 155 160

Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg
 165 170 175

Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro
 180 185 190

Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly
 195 200 205

Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr
 210 215 220

Asn Asp Ile Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly
 225 230 235 240

Gly Thr Thr Glu Tyr Pro Tyr Pro Arg Arg Gly Arg Thr Gly Arg Pro

				245						250					255	
Arg	Ser	Arg	Arg	Asp	His	Asn	Tyr	Glu	Ser	Arg	Leu	Ser	Pro	Ile	Met	
			260					265					270			
Ser	Leu	Asp	Ile	Tyr	Val	Pro	Lys	Asp	Glu	Asn	Phe	Gly	His	Leu	Lys	
		275					280					285				
Met	Ser	Asp	Phe	Leu	Gly	Tyr	Thr	Leu	Lys	Ala	Leu	Ser	Ile	Ser	Ile	
	290					295					300					
Lys	Pro	Gly	Leu	Gln	Ser	Ile	Phe	Asp	Val	Thr	Pro	Asn	Glu	Phe	Asp	
305					310					315					320	
Asn	Phe	Lys	Glu	Val	Asp	Asn	Leu	Phe	Glu	Arg	Gly	Phe	Pro	Ile	Pro	
				325					330					335		
Phe	Asn	Ala	Phe	Lys	Thr	Leu	Thr	Glu	Asp	Leu	Thr	Pro	Pro	Leu	Phe	
			340					345					350			
Lys	Ala	Leu	Val	Arg	Asn	Asp	Gly	Glu	Lys	Phe	Leu	Lys	Phe	Pro	Thr	
		355					360					365				
Pro	Glu	Val	Val	Lys	Asp	Asn	Lys	Ile	Gly	Trp	Ser	Thr	Asp	Glu	Glu	
	370					375					380					
Phe	Ala	Arg	Glu	Met	Leu	Ala	Gly	Pro	Asn	Pro	Leu	Leu	Ile	Arg	Arg	
385					390					395					400	
Leu	Glu	Ala	Phe	Pro	Pro	Thr	Ser	Lys	Leu	Asp	Pro	Asn	Val	Tyr	Gly	
				405					410					415		
Asn	Gln	Asn	Ser	Thr	Ile	Thr	Glu	Glu	His	Ile	Lys	His	Gly	Leu	Asp	
			420					425					430			
Gly	Leu	Thr	Val	Asp	Glu	Ala	Met	Lys	Gln	Asn	Arg	Leu	Tyr	Ile	Val	
		435					440					445				
Asp	Phe	His	Asp	Ala	Leu	Met	Pro	Tyr	Leu	Thr	Arg	Met	Asn	Ala	Thr	
	450					455					460					
Ser	Thr	Lys	Thr	Tyr	Ala	Thr	Arg	Thr	Leu	Leu	Leu	Leu	Lys	Asp	Asp	
465					470					475					480	
Gly	Thr	Leu	Lys	Pro	Leu	Val	Ile	Glu	Leu	Ala	Leu	Pro	His	Pro	Gln	
				485					490					495		
Gly	Asp	Gln	Leu	Gly	Ala	Ile	Ser	Lys	Leu	Tyr	Phe	Pro	Ala	Glu	Asn	
			500					505					510			
Gly	Val	Gln	Lys	Ser	Ile	Trp	Gln	Leu	Ala	Lys	Ala	Tyr	Val	Thr	Val	
		515					520					525				
Asn	Asp	Val	Gly	Tyr	His	Gln	Leu	Ile	Ser	His	Trp	Leu	His	Thr	His	
	530					535					540					

Ala Val Leu Glu Pro Phe Val Ile Ala Thr His Arg Gln Leu Ser Val
 545 550 555 560
 Leu His Pro Ile His Lys Leu Leu Val Pro His Tyr Lys Asp Thr Met
 565 570 575
 Phe Ile Asn Ala Ser Ala Arg Gln Val Leu Ile Asn Ala Asn Gly Leu
 580 585 590
 Ile Glu Thr Thr His Tyr Pro Ser Lys Tyr Ser Met Glu Leu Ser Ser
 595 600 605
 Ile Leu Tyr Lys Asp Trp Thr Phe Pro Asp Gln Ala Leu Pro Asn Asn
 610 615 620
 Leu Met Lys Arg Gly Leu Ala Val Glu Asp Ser Ser Ala Pro His Gly
 625 630 635 640
 Leu Arg Leu Leu Ile Asn Asp Tyr Pro Phe Ala Val Asp Gly Leu Asp
 645 650 655
 Ile Trp Ser Ala Ile Lys Thr Trp Val Gln Asp Tyr Cys Cys Leu Tyr
 660 665 670
 Tyr Lys Asp Asp Asn Ala Val Gln Asn Asp Phe Glu Leu Gln Ser Trp
 675 680 685
 Trp Asn Glu Leu Arg Glu Lys Gly His Ala Asp Lys Lys His Glu Pro
 690 695 700
 Trp Trp Pro Lys Met Gln Thr Leu Ser Glu Leu Ile Glu Ser Cys Thr
 705 710 715 720
 Thr Ile Ile Trp Ile Ala Ser Ala Leu His Ala Ala Val Asn Phe Gly
 725 730 735
 Gln Tyr Pro Tyr Gly Gly Tyr Ile Leu Asn Arg Pro Thr Thr Ser Arg
 740 745 750
 Arg Phe Met Pro Glu Val Gly Thr Ala Glu Tyr Lys Glu Leu Glu Ser
 755 760 765
 Asn Pro Glu Lys Ala Phe Leu Arg Thr Ile Cys Ser Glu Leu Gln Ala
 770 775 780
 Leu Val Ser Ile Ser Ile Ile Glu Ile Leu Ser Lys His Ala Ser Asp
 785 790 795 800
 Glu Val Tyr Leu Gly Gln Arg Ala Ser Ile Asp Trp Thr Ser Asp Lys
 805 810 815
 Ile Ala Leu Glu Ala Phe Glu Lys Phe Gly Lys Asn Leu Phe Glu Val
 820 825 830
 Glu Asn Arg Ile Met Glu Arg Asn Lys Glu Val Asn Leu Lys Asn Arg
 835 840 845

Ser Gly Pro Val Asn Leu Pro Tyr Thr Leu Leu Val Pro Ser Ser Asn
850 855 860

Glu Gly Leu Thr Gly Arg Gly Ile Pro Asn Ser Ile Ser Ile
865 870 875